

Genetic variability studies for yield and yield components in groundnut (*Arachis hypogaea* L.)

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ABSTRACT

The present study was aimed to assess genetic variability for yield and yield component traits among 100 released Indian groundnut varieties and were evaluated during post rainy season (January-June) 2023-24 at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru, Hyderabad. The analysis of variance revealed significant differences among the varieties for all the traits suggesting that the varieties had very good diversity and will provide valuable insights. The genetic parameters revealed very good amount of genetic variability for exploitation. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for the traits, pod yield (kg/ha), kernel yield (kg/ha), oleic acid (%) and linoleic acid (%) suggesting substantial variability that can be utilized in breeding programs. The traits, oleic acid (%) and linoleic acid (%) showed high heritability and high genetic advance as percentage of mean, implying that the heritability is likely due to additive gene effects and simple selection is effective for the improvement of these traits.

Key words: Coefficient of variation, Genetic advance, Groundnut, Heritability and Variability

Groundnut also known as earhnut, peanut, goober, or the “poor man’s nut,” is a nutritious oilseed and legume crop. It earns the “poor man’s nut” label because it offers high protein and fat content similar to that of cashew nuts, but at a lower price, making it more accessible for those with limited resources. In India, groundnut is cultivated in 5.7 million hectares, yielding an average of 1,776 kg per hectare and resulting in a total production of 10.1 million tonnes. Worldwide, groundnut is grown on 30.5 million hectares, with the same yield rate, leading to a global production of 54.2 million tonnes (FAO STAT, 2022).

Groundnut (*Arachis hypogaea* L.) is an annual herb belongs to the Fabaceae (Leguminosae) family. It is categorized into two subspecies: subsp. *fastigiata* Waldron and subsp. *hypogaea* Krap. Subsp. *fastigiata* includes four botanical varieties: var. *vulgaris*, var. *fastigiata*, var. *peruviana*, and var. *aequatoriana*, while subsp. *hypogaea* consists of two varieties: var. *hypogaea* and var. *hirsuta*. Each of

these varieties displays unique characteristics in terms of plant, pods, and seeds (Krapovickas and Gregory, 1994). Groundnut is an allotetraploid with a chromosome number of $2n = 4x = 40$, featuring “AA” and “BB” genomes. Among groundnut species, *A. hypogaea* and *A. monticola* in section *Arachis*, as well as some species in section *Rhizomatosae*, are allotetraploids, whereas other species are diploids with $2n = 2x = 20$ chromosomes. The donor of the ‘AA’ genome in cultivated groundnut is *A. duranensis*, while *A. ipaensis* serves as the donor of the ‘BB’ genome (Kochert *et al.*, 1996).

The potential for crop improvement relies on the variability present in yield and yield-related traits. Heritability and genetic advance provides insights into how genetic factors influence the expression of these traits. In groundnut, huge variability is existed and it can be exploited in the breeding programmes. At the same time, hundreds of varieties for various traits are released for commercial cultivation over a period.

Therefore, an effort was made in the present study to assess the nature and extent of genetic variability in the released varieties of India.

MATERIAL AND METHODS

In the present study 100 Indian released groundnut varieties were evaluated in an alpha lattice design with two replications during the post rainy season (January-June) 2023-24 at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad. Each genotype was planted in two rows of 4.0 meters length with a spacing of 30 cm between rows and 10 cm between plants within the rows. Data were collected on various traits, including days to first flowering (DFF), days to 50% flowering (DFPF), percentage of mature pods (PMP), hundred kernel weight (HKWT), shelling percentage (SP), stearic acid (%) (SAVSA), palmitic acid (%) (PAVPA), oleic acid (%) (OAVOA), linoleic acid (%) (LAVLA), pod yield in kg/ha (PYKH), and kernel yield in kg/ha (KYKH).

The analysis of variance was conducted using the method proposed by Williams and Patterson (1977), while the genotypic and phenotypic coefficients of variation were estimated as per the approach suggested by Burton and Devane (1953). Data analysis was performed using R Studio software (version R-4.4.1). The GCV and PCV were categorized as low (< 10%), moderate (10-20%) and high (> 20%) based on the classification given by Sivasubramanian and Menon (1973). Heritability was calculated using the formula provided by Johnson *et al.* (1955), which classifies heritability as low (below 30%), moderate (30-60%) and high (above 60%). The range of genetic advance as a percentage of mean was also classified as low (< 10%), moderate (10-20%) and high (> 20%) according to Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance for eleven characters, revealed significant differences among the genotypes for all the characters included under study indicating the presence of greater variability among the genotypes (Table 1). The genetic variability parameters of all the traits are presented in Table 2. Low GCV and PCV (<10%) values were recorded for the traits *viz.*, days to first flowering, days to 50 % flowering, percentage of

mature pods (%), shelling percentage (%) and palmitic acid (%) indicating that the variability for these characters among the genotypes was meagre. Similar results were reported by Kumari and Sasidharan (2020), Gali *et al.* (2021), Veer and Kumar (2021), Gangadhara and Gor (2022) and Shendekar *et al.* (2023).

The characters, pod yield (kg/ha), kernel yield (kg/ha), oleic acid (%), linoleic acid (%), registered higher GCV and PCV (>20%) values indicating that large amount of variation is present among the genotypes for these characters. Similar results were obtained by Vekariya *et al.* (2011), Patidar and Nadaf (2017), Mohapatra and Khan (2020), Gali *et al.* (2021), Veer and Kumar (2021) and Shendekar *et al.* (2023).

High heritability coupled with high genetic advance as per cent of mean (Table 2) was noted for oleic acid (%) and linoleic acid (%), indicating that these traits are mostly under the control of additive gene action and hence direct phenotypic selection of these traits would be effective for improvement. Similar findings were earlier reported for these characters by Mohapatra and Khan (2020) and Gali *et al.* (2021) for oleic acid (%) and Gali *et al.* (2021) and Suresh *et al.* (2021) for linoleic acid (%).

High heritability coupled with moderate genetic advance as per cent of mean was observed for the traits *viz.*, stearic acid (%) and palmitic acid (%) indicating the presence of both additive and non-additive genetic effects and genetic improvement of these characters can be exploited through heterosis breeding. Similar finding was earlier reported by Gali *et al.* (2021) in groundnut.

CONCLUSION

High PCV and GCV were recorded for the traits *viz.*, pod yield (kg/ha), kernel yield (kg/ha), oleic acid (%), linoleic acid (%) indicating that the large amount of variation in 100 released varieties. High heritability coupled with high genetic advance as per cent of mean was recorded for the traits like oleic acid (%) and linoleic acid (%) indicating that these traits were under the control of additive gene action and hence direct phenotypic selection of these traits would be effective for the improvement of these traits in groundnut.

Table 1. Analysis of variance for yield and yield components in groundnut (*Arachis hypogaea* L.)

Source of Variation	d.f	DFF	DFPF	PMP	HKWT	SP	SAVSA	PAVPA	OAVOA	LAVLA	PYKH	KYKH
Replication	1	13.52	2.65	0.59	0.13	22.29	0.05	0.02	4.65	8.73	1139423.3	630029.93
Genotype	99	5.89**	10.60**	40.03*	78.78**	35.51**	0.13**	2.83**	164.32**	125.71**	529880.97**	280493.51**
Block (Replication)	18	0.88	1.77	20.33	58.14	15.23	0.02	0.4	12.95	10.02	353767.52	226091.54
Error	81	0.97	1.57	27.99	22.15	9	0.02	0.18	9.33	7.03	145342.67	88213.03

* Significance at 5% level, ** Significance at 1% level

Characters: Days to first flowering (DFF), days to 50% flowering (DFPF), percentage of mature pods (PMP), hundred kernel weight (HKWT), shelling percentage (SP), stearic acid content (SAVSA), palmitic acid content (PAVPA), oleic acid content (OAVOA), linoleic acid content (LAVLA), pod yield in kg/ha (PYKH), and kernel yield in kg/ha (KYKH).

Table 2. Estimates of variability, heritability and genetic advance as per cent of mean for yield and yield component traits in groundnut (*Arachis hypogaea* L.)

S. No.	Character	Coefficient of		Heritability (%) (broad sense) (h^2)	Genetic advance as per cent of mean (%) (GAM)
		GCV (%)	PCV (%)		
1	Days to first flowering (days)	4.51	5.31	72.08	7.89
2	Days to 50 % flowering (days)	5.6	6.52	73.71	9.9
3	Percentage of mature pods (%)	3.01	6.77	19.75	2.75
4	Hundred kernel weight (g)	14.56	21.23	47	20.56
5	Shelling per cent (%)	4.79	6.67	51.56	7.09
6	Stearic acid (%)	8.64	10.4	68.95	14.77
7	Palmitic acid (%)	8.4	9.11	84.98	15.95
8	Oleic acid (%)	22.09	23.48	88.46	42.8
9	Linoleic acid (%)	21.17	22.49	88.52	41.02
10	Pod yield (kg/ha)	21.88	31.47	48.36	31.35
11	Kernel yield (kg/ha)	21.53	32.94	42.73	28.99

PCV - Phenotypic coefficient of variation; GCV - Genotypic coefficient of variation

ACKNOWLEDGEMENTS

The first author is highly grateful to ANGRAU for providing stipend during the M.Sc(Ag) programme and ICRISAT for extending the facility to carryout the experiment.

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